## SEARCH REQUEST FORM

Scientific and Technical Information Center

	Requester's Full Name: BRUC	e billion ledeschi	Examiner #: 78/50	Date: $\frac{2\sqrt{\sqrt{a_1}}}{2}$
/	Art Unit: 1642 Phone N	Number 30 6 - 4 8 2 7	Serial Number: 7.97	401900
7	Mail Box and Bldg/Room Location	Resi	ults Format Preferred (circle)	: PAPER DISK E-MAIL
2	If more than one search is subm	nitted, please prioritiz	ze searches in order of no	ed.
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	include the elected species or structures, k	eywords, synonyms, acror	lyms, and registry numbers, and o	combine with the concept or
_	utility of the invention. Detine any terms	that may have a special me	caning. Give examples or relevan	it citations, authors, etc, if
	known. Please attach a copy of the cover s			
	Title of Invention: FAMILY of t	TAMMALIAN POTI	ossium chesally The	in cloning
	Inventors (please provide full names): _	FLURION LUSAGE	ERIC GUILLEMARE	Michael Fink
	FARRICE DUPLAT Ct c			
	Earliest Priority Filing Date:	11,2000		
	*For Sequence Searches Only* Please includ appropriate serial number.	le all pertinent information (	parent, child, divisional, or issued p	atent numbers) along with the
	SEQ IDAI			
	SEQ 104	2		
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	STAFF USE ONLY	Type of Search		
	Searcher:	NA Sequence (#)	STN	•
	Searcher Phone #:	AA Sequence (#)	Dialog	
	Searcher Location:	Structure (#)	Questel/Orbit	
	Date Searcher Picked Up:	Bibliographic	Dr.Link	
	Date Completed: 2/2/6/	Litigation	Lexis/Nexis	100
	Searcher Prep & Review Time:	Fulltext	Sequence Systems <u>QDSS</u>	
	Clerical Prep Time:	Patent Family	WWW/Internet	
	Online Time:	Other	Other (specify)	-

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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/gene="HOO1"
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/note="similar to d-ORK product rectifier/leak potassium
channel subunit with four predicted transmembrane
channel subunit with four predicted transmembrane
segments; named HOHO1 for Human ORK-homologous open
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product, TWIK1, encoded by GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSV
ELPYEDLLRQELRKLKRFLEBHECLSFQQLEQFLGRVLEASRYGVSVLSNASGNWNW
DETSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVGIFFTLLFLTAVVQRITVHV
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/dev_stage="3 months old infant"
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Query Match Best Local Sim Matches 1224;

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64.6%; ilarity 100.0%; Conservative

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Score 1224; pred. No. 2.2 0; Mismatches

DB 53; 2.2e-165;

Length Indels

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U90065
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Desir,G.V., Orias,M. and
The cloning of a human po
Unpublished
                                                                                                                                                                                                                                                           Submitted (19-FEB-1997) Internal Cedar St., New Haven, CT 006510,
                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                    Desir, G.V., Orias, M.
                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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                                    /translation="MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLYLVFGAVVFSSV
ELPYEDILTROELRKLKRFFLEBHECLSEQOLEOFLGRVLEASRYGVSVLSNASGNWNW
DFTSALFFASTVLSTTGYGHTVPLSDGGKAFC I IYSVI FIDFTLLFLTAVVQRITVYN
TRRPYLYFHIXWGFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDDWHFLESFYF
CFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIAMLVVLETFCELHELKKF
CKMFYVKKDKDEDQVHIIEHDQLSFSSITDQAAGMKEDQKQNEPFVATQSSACVDGPA
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
183. .1193
                                                                                                                     /product="potassium channel
/protein_id="AAB51147.1"
/db_xref="GI;1916295"
                                                                                                                                                              /note="DPK; has two
/codon_start=1
                                                                                                                                                                                                                                            Location/Qualifiers
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Eutheria; Primates;
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Catarrhini; Hominidae
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CCTTCTCCTCGATCACAGACCAGGCAGCTGGCATGAAAGAGG.ACCAGAAGCAAAATGAGC
                                     TCTATGTGAAGAAGGACAAGGACGAGGATCAGGTGCACATCATAGAGCATGACCAACTGT
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                             TCTATGTGAAGAAGGACAAGGACGAGGATCAGGTGCACATCATAGAGCATGACCAACTGT
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25 musculus TWIK-1 K+ c.

AF033017 U86009

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3 (bases
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Submitted (05-NOV-1997) IPMC, CNRS,
                                                                                                                                                                                                                                                                                                                                         Valbonne 06560, France
On May 23, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2240)
Arrighi, I., Lesage, F.,
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Mammalia; Eutheria; Roder
1 (bases 1 to 2240)
Lesage, F., Lauritzen, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 425
                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse
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                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               hi,I., Lesage,F., Scimeca,J.C.,
ture, chromosome localization, a
twik K+ channel gene
Lett. 425 (2), 310-316 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse.
                                                                                                                                                                       /product="TWIK-1 K+ channel"
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DFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTALVQRVTVHV
                                                                                                                          DH
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CFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLITMLVVLETFCELHELKKF
                                                                                                                                    {\tt RKMFYVKKDKDEDLVHIMEHDQLSFSSVTEQVAGLKEEQKQSEPFVASQSPPYEDGSA}
                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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            TTTAAGAAATAGCTACTGTTTGCAATGTCTTATTAAAAAACAACAACAAAAAAAGACACACTGG
                                AGAGGCAGAGTCTTGACTGCATCCATTTTCAAAAGAAAGTCAAAGCTAAGATGATGTTAT
                                          CAAGGAAGAGGCTTAAGTATGTTCATTTTTATCAGAATGCAAAAGCGAAAAGTTATGTCAC
                                                                           CCCTGCAAACCATTGAGGCGTAGGATTTGTTGCATTATGCTAGAGCACCAGGGTCAGGGTG
                                                                                                    GGAGGAGCAGAGCAAAGTGAGCCTTTTGTGGCCTCCCAGTCCCCACCCTATGAGGATGG
                                                                                                            CCTGCTACTTGGCCTTATTGCCATGTTGGTAGTTCTGGGAAACCTTCTGTGAACTCCATGA 997
                                                                      CTCTGCAGACCACTGAGTGTGGG
                                                                                                                                                                       GCTGAAGAAGTTCAGGAAGATGTTCTACGTGAAGAAAGACAAGGACGAAGACCTGGTTCA
                                                                                                                                                                                GCTGAAAAAATTCAGAAAAATGTTCTATGTGAAGAAGGACAAGGACGAGGATCAGGTGCA 1057
                                                                                                                                                                                                        CCTGCTCCTCGGACTCATCACCATGCTGGTTGTCCTGGAGACCTTCTGTGAACTCCACGA 1105
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KEYWORDS
SOURCE
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VERSION
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
Conterproject Information
Center project name: dJ550p15
Center project name: XGAP4; version 4.5
Sasembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 29% of reads
Dye-terminator Big Dye; 70% of reads
Consensus quality: 119154 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTTCTCTTTATACTAAAGAATCCAGAGTTGCTACAATAAAATAAAGGGGAATAATAAAA 1883
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                                                                                                                                                                  Direct Submission

Direct Submission

Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 6, 2000 this sequence version replaced gi:10045423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GCAGTATGCTGCTGTGGTTAGAAGCAGATTTTATACTTTTAACTGGAAACTTTGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                     ALJ356357 119793 bp DNA
Homo sapiens chromosome 1 clone i
PROGRESS ***, 3 unordered pieces
ALJ356357
                                                                                                                                                             Center code:
                                                                                                                                                                                                                                                                                    Donnelly, S.
                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                                                        AL356357.12 GI:10715989
                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                   (bases
                                                                                                                                                                                                                                                                                               ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 119793)
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                                 reads
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                                Chemistry:
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BASE COUNT
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                                      CGTGGATGGCCCTGCAAACCATTGAGCGTAGGATTTGTTGCAT FATGCTAGAGCACCAGG
                                                                                                                                               CGTGGATGGCCCTGCAAACCATTGAGCGTAGGATTTGTTGCATIATGCTAGAGCACCAGG
                                                                                                                                                                                                                                                  TGGCATGAAAGAGGACCAGAAGCAAAATGAGCCTTTTGTGGCCACCCAGTCATCTGCCTG
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Insert size: 137798; 10.4% error; agarose-fp
Quality coverage: 9.92x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coverage: 8.61x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70525 115446: conti
115447 115546: gap of
115547 119793: cont
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70425 70524: gap of 100 bp
70525 115446: contig of 44922 bp in length
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clone_end:T7
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fragment_chain:1"
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fragment_chain:1"
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/clone_lib="RPCI-4"
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/db_xref="taxon:9606"
/chromosome="1"
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              RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Eoglymore, A., Costle, A., Choepel, Y., Colangelo, M., Collins, S., Campopiano, A., Costle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grandt, P., Grant, G., Hayos, B., Haeford, A., Horton, L., Grandt, P., Grant, G., Hayos, B., Haeford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Polsani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, C., P., Rothman, D., P., Rothman, P., P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E Homo sapiens chromosome 1, clone RP11-274P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome SEQUENCE, 23 unordered p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Pr
1 (bases 1 to 172020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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AC025873.3 GI:8099837
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1 clone
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RP11-274P19
Riley, R.,
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  Rogov, P.,
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     Rothman, D
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COMMENT JOURNAL

Young, G.,

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bp in

length

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Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 28, 2000 this sequence version replaced gi:7651989. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy.A., Santos.R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 160532 bases at least Q30 Consensus quality: 166374 bases at least Q30 Consensus quality: 166374 bases at least Q30 Consensus quality: 168374 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 171000; agarose-fp
Insert size: 169820; sum-of-contlys
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L8005
Center clone name: 274_P_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
                          50543 50642: gap of 100 pp
50643 60925: contig of 10283 bp in length
                                                                                                                                                                                           25349 25448: gap of 100 bp
25449 31428: contig of 5980 bp in
                                                                                                                                                                                                                                                             21785 21884:
                                                                                                  14572 44671:
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14968 17745; contig of 2778 bp in
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2718 40
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1172 1271: gap of 100 bp
1272 2617: contig of 1346 bp in length
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0035: contig of 1
36 6135: gap of 100
16 8540: contig - 7
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                                                                                                                                                                                                                                                                           18990: gap of 100 bp
21784: contig of 2794 bp in
                                                                                                                                         38231:
                                                                                                                                                                                 31528:
                                                                                                                                                                                                                                                                                                                                                                                                                       11232:
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                        61025:
                                                                                                                                                                                                                                  25348: con+
                                                                                                                                                        38131: contig of 6603 bp in length
                                                                            571: gap of 100 bp
50542: contig of 5871 bp in length
                                                                                                                 131: gap of 100 bp
44571: contig of 6340 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                      15: gap of 100 bp
8540: contig of 2405 bp in
10: gap of 100 bp
11132: contig of 2492 bp in
                                                                                                                                                                                                                                                                                                                45: gap of 100 bp
18890: contig of 1045 bp in length
                                                                                                                                                                                                                                                                                                                                                                                              32: gap of 100 bp
14867: contig of 3635 bp in
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                      gap of
                                                                                                                                                                                                                                    ap of 100 bp
contig of 3464 bp in
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f 1837 bp in
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Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 167120 bases at least Q40
Consensus quality: 17054 bases at least Q30
Consensus quality: 171743 bases at least Q20
Insert size: 173229; sum-of-contigs
Insert size: 185723; 5.5% error; agarose-fp
Ouality coverage: 4.5x in Q20 bases; sum-of-contigs
coverage: 4.21x in Q20 bases; agarose-fp
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AL360006
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On Sep 16, 2000 this sequence versi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-SEP-2000) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burton, J
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HTG; HTGS_PHASE1; HTGS_DRAFT
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             152697 157665: contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmalia; Metazoa; Chordata;
mmalia; Eutheria; Primates;
(bases 1 to 174629)
                                                                                                                                            110565 110664: gap c
110665 132215: con
132216 132315: gap c
132316 134650: con
                                                                         134751 132596; contig of 17846 b
152597 152666; gap of 17846 b
152597 152667; gap of 100 km
                                                                                                                                                                                                       85950 86049: gap of 100 bp

86050 93827: contig of 7778 b

93828 93927: gap of 100 bp

93928 102074: contig of 8147 b

102075 102174: gap of 100 bp

102175 110564: contig of 8390 b
                                                                                                                                                                                                                                                                                                       25353 25452: gap of 100 bp 25453 65850: contig of 40398 bp in length 65851 65950: gap of 100 bp 65951 75622: contig of 9672 bp in length 75623 75722: gap of 100 bp 75723 85949: contig of 10227 bp in length 85650 66606 9672 bp in length
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85950 86049:
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                                                                                                                           134650: cc 34750
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                                                                               Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                Kaczmarek, L.K.
Cloning and localization
with two P domains
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AF022819.1
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2 (bases 1
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Gan, L., Joiner, W.J.,
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                                                                                                                                                                   bp mRNA ROD
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                                                                                ; Chordata; ; Rodentia;
                                                Quinn, A.M., Wang, L.-Y.,
                              of.
                              rTWIK,
                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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TWIK mRNA, complete
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Kaczmarek,L.K.
Direct Submission
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University, 333 Cedar St.,
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Cloning and nephron segment localization of a
channel, KCNK1: exclusive distal expression
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WDFASALFFASTVLSTTGYGHTVPLSDVGKAFCIIYSVLGIPFTLLFTTAVVQRVTVH
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                                                                                                                                                                                                                       TTG 957
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                                         Homo sapiens chromosome 1 clon
SEQUENCE, 23 unordered pieces.
ACO25873
                      AC025873.3 GI:8099837
                                                                                             AC025873
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91.2%;
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Pred. No. 3.4e-85;
0; Mismatches 66
                                                                   VA HTG
clone RP11-274P19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE 2 (bases 1 to 172020)

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Basten,V., Beda,F., Anderson,S., Baldwin,J., Barna,N., Bastlen,V., Beda,F., Boyuslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., McCarthy,M., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T., Mihova,T., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trajilio,J., Vossiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16 MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 28, 2000 this sequence version replaced gi:7651989. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                 Center project name: L8005

Center clone name: 274_P_19

Center clone name: 274_P_19

Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry program: Phrap; version 0.960731

Consensus quality: 160532 bases at least 040

Consensus quality: 166189 bases at least 030

Consensus quality: 168374 bases at least 020

Insert size: 171000; agarose-fp

Insert size: 169820; sum-of-contigs
                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cre
Mammalla; Eutheria; Primates; Cat
1 (bases 1 to 172020)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome Unpublished
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                                                                     1172 1271: gap
1272 2617:
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 9 4198: gap 6035:
                            2617: contig of 1346 bp
2717: gap of 100 bn
4098: conti-
                                                                                         1171: contig
1: gap of
p of 100 bp: contig of 1381 bp i 100 bp cf 100 bp: contig of 1837 bp i
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                                                                                                      of 1171 bp
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1 Q20 bases;
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18991 21784: contig of 2794 bp ir

21785 21884: gap of 100 bp

21885 25348: contig of 3464 bp in

25349 25448: gap of 100 bp

31428: contig of 5980 bp in

31429 31528: gap of 100 hp
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31529 38131: contig of 6603 bp in length
38132 38231: gap of 100 bp
38232 44571: contig of 6340 bp in length
44572 44671: gap of 100 bp
50543: 50542: contig of 5871 bp in length
50543: 50642: gap of 100 bp
50643: 60925: contig of 10283 bp in length
60926: 61025: gap of 100 bp
61026: 71074: contig of 10049 bp in length
71075 71174: gap of 100 bp
71175 82308: contig of 11134 bp in length
82309 82408: gap of 100 bp
82409 92547: contig of 10139 bp in length
92548 92647: gap of 100 bp
109898 109997: gap of 100 bp
109898 109997: gap of 100 bp
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6136 8540: contig of 2405 bp
8541 8640: gap of 100 bp
8641 11132: contig of 2492 bp
11133 11222: gap of 100 km
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14968 17745: contig of 2778 l
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18890: contig of 1045 k
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ORIGIN
                                                       Query Match 26.6%;
Best Local Similarity 95.9%;
Matches 532; Conservative
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                                                                                                      CGACGCTTCTTGGAGGAGCACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGCTTCCTGGGC 422
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               GGCCACACCGTGCCC
                              AACTGGGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTAT
                                                                                             CGACGCTTCTTGGAGGAGCACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGC
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                                                                                                                                                                    TGGTGCTTCCGCCTCCTGGTGCTGGGCCTACCTTGCTCTACCTGGTCTTCCGCCCAGTGGTC 302
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ACACGACCCCACTGACGGATGCAGGCAAAGCCTTCTCCATCGTTTTTGCACTCCTGGGCG
             ACACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCA 606
                                                                                                                                                                                                                                                TGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGC 321
                                             GGGACTTTGCCTCGGCGCTCTTCTTCGCCAGCACGCTAGTCACCACCATGGGCTATGGCT
                                                           GGGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCC 546
                                                                                          GGCTGGGGCGCAGTGCTGGCCAACGCATCGGGACCCCGCCAACGCTTCGGACCCCGCGT
                                                                                                          GCCCGTGCGTGGCGGCTCACGCCCTGGACGCCTTCGTGGAGCGGGTGCTGGCGGCAGGAC 211
                                                                                                                                                      ACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCA 441
                                                                                                                                                                                                   CGCACGAAGCCCGGCTGCGGGCAGAGCTGGGGGACGCTGCGGGAGCAGCTGCTGCGGCACA 151
                                                                                                                                                                                                                                                                                    474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUN-2000) Institut Cellulaire-CNRS, 660, Route des I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2243)
Patel, A.J., Maingret, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TWIK-2, an inactivating ;
J. Biol. Chem. 275 (37),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 2243)
Patel, A.J., Maingret, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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Pred. No. 1.4e-29;
0; Mismatches 298;
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Sciurognathi; Muridae; Murinae;
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Lucioles, Valbonne 06560, Fran
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TWIK-2 mRNA, complete
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                                                                                                                                                                                      Primer A: GGTCCTCTACTTCCACAT
Primer B: GCTCTCTGAATTTTTGATT
STS size: 239
PCR Profile:
                                                                                                                                                                                                                                                          Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                              human 9
G20759
Buffer:
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STS; STS sequence;
                                                                                                 Protocol:
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                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                     Primer:
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Total Volume:
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A006F14,
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sequence; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                               CGTGCTCCTTGGGGTTTGTCACTGTGTCCTGCTTCTYCTTCATCCCGGCCGCTGTCTTCTC
                                                                                                                                                                                                                                                            Homo sapiens 2P domain K+ channel TWIK-2 (KCNK6) mRNA, cds, alternatively spliced.
                                                                                        Direct Submission
Submitted (23-JUN-2000) Institut
Cellulaire-CNRS, 660, Route des J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prepared with primer pairs derived Accession Numbers F06938, F12504, Location/Qualifiers
                                                                                                                             2 (bases 1 to 1017)
Patel, A.J., Maingret, F.,
                                                                                                                                                                                   Patel, A.J., Maingret, F.,
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini: Hominidae; Homo.
                                                                                                                                                                                                                                   human
                                                                                                                       Honore, E.
                                                                                                                                                                    TWIK-2,
                                                                                                                                                                                                                           Homo
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                                                                                                                                                                              Honore, E.
                                                                                                                                                           Biol. Chem.
                                                                                                                                                                                              (bases 1 to 1017)
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                                                                                                                                                         an inactivating : . Chem. 275 (37),
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1. .18
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Triton X-100:
Concentration:
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/note="TWIK-2"
76. .1017
                                  /map="19q13.1"
                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                   /gene="KCNK6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                   location/Qualifiers
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99.6%;
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Pred. No. 7.7e-25;
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                       AGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGT
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/protein_id="AAG10506.1"
//db_xref="G1:9971945"
//tanslation="MRGALLAGALAAYAAYLYLGALLVARLEGPHEARLRAELETLR
AQLLQRSPCVAAPALDAFVERVLAAGRLGRVVLANASGSANASDDAWDFASALFFAST
LITTVGYGYTTPLTDAGKAESIAFALLGVPTTMLLLTASAQRLSLLTHVDLSWLSMR
WGWDPRAACWHLVALLGVVVTVCFLVPAVIFAHLEEAWSFLDAFYFCFISLSTIGLG
DYVPGEAPGQDYRALYKVLYTYVLFLGLVAWULVLQTFRHVSDLHGLTELILLPPPCP
ASFNADEDDRVDILGPQPESHQQLSASSHTDYASIPR"

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CTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTGTTTTATTTC
                          GCACTTGGTGGCCCTGTTGGGGGTCGTAGTGACCGTCTGCTTTCTGGTGCCGGCTGTGAT
                                                 CCATGCCGTGCTTCGTTTGGTTACTGTGTCTTCTTCTTCTTCATCCCGGCCGCTGT
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